



## ATTACHMENTS:

### 1) Corrected Sequence Listing



1

SEQUENCE LISTING

<110> ASAKO, HIROYUKI  
MATSUMURA, KENJI  
SHIMIZU, MASATOSHI  
ITO, NOBUYA  
WAKITA, RYUHEI

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE  
4-HALO-3-HYDROXYBUTANOATE

<130> 7372-72249

<140> 10/004,115  
<141> 2001-12-06

<150> JP 2000-372704  
<151> 2000-12-07

<150> JP 2001-006144  
<151> 2001-01-15

<150> JP 2001-026594  
<151> 2001-02-02

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<151> 2001-06-11

<160> 37

<170> PatentIn Ver. 3.2

<210> 1  
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<213> Penicillium citrinum

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Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr  
20 25 30

Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp  
35 40 45

Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg  
50 55 60

Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val  
65 70 75 80

Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp  
85 90 95

Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met  
100 105 110

Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu  
 115 120 125  
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr  
 130 135 140  
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp  
 145 150 155 160  
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu  
 165 170 175  
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile  
 180 185 190  
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe  
 195 200 205  
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn  
 210 215 220  
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn  
 225 230 235 240  
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala  
 245 250 255  
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro  
 260 265 270  
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp  
 275 280 285  
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val  
 290 295 300  
 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala  
 305 310 315 320  
 Lys Asn Leu Ser Ala  
 325

<210> 2  
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 <213> *Penicillium citrinum*

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 1 5 10 15

ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc	96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	
20 25 30	
tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac	144
Tyr Thr Ala Val Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	
35 40 45	
tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	
gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	
tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	
tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
100 105 110	
ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	
ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
130 135 140	
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
145 150 155 160	
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
165 170 175	
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
180 185 190	
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
195 200 205	
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
210 215 220	
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
225 230 235 240	

gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala	
245	250
255	
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	
260	265
270	
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac	864
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp	
275	280
285	
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc	912
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val	
290	295
300	
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc	960
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala	
305	310
315	320
aag aac ctg tct gcg tga	978
Lys Asn Leu Ser Ala	
325	

&lt;210&gt; 3

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Penicillium citrinum

&lt;400&gt; 3

Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn Gln Val	
1	5
10	
15	

Pro

&lt;210&gt; 4

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Penicillium citrinum

&lt;400&gt; 4

Ile Pro Gly Val Phe Gly Thr Phe Ala Ser	
1	5
10	

&lt;210&gt; 5

&lt;400&gt; 5

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&lt;210&gt; 6

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Penicillium citrinum

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<222> (6)..(7)
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<400> 6
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1           5           10

<210> 7

<400> 7
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<210> 8
<211> 20
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<220>
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<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> a, c, t, g, other or unknown

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tangcnacng gcataatatt                                         20

<210> 10
<211> 20
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<400> 11
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20

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<210> 12
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<220>
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<400> 12
tangcnacng gcatgatgtt
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20

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<210> 13
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<212> DNA
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<220>
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<400> 13
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<210> 14
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer
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agtgaagggtt ccaagggcga aacctatnct gctgtcacca ctgcccctgaa aaccgggttac 180
cgtncttgg actgtgcctg gtactacctg aacaagggtg aggttggtga gggtnccgt 240
gacttcctga aggaaaaccc ctcgggtgaag cgtgaggaca tcttcgtctg caccagggtg 300
tggaaaccacc tccaccgtta tgaggacgtc ctctggtcca ttgacnactc cctgaagegt 360
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```

cttggacttg actacgttga tatgttcctc gttcaactggc ccattgctgc cgaaaaaaaaat 420
ggccagggtg agccccaaaat tggccctgac ggcaaatacn tcnttctcaa ggacctgacc 480
gaaanccna ncccacctgg cgcgctatgg aaaaaatttn tgangatccc aaggccaggt 540
ccatgggtgt ttccaatttg accattgccc accttgagaa gatgtccaag ttngccaagg 600
tnatgcctca cgccaaccag atcgagattc acccccttct gcccaacgag gagctggtgc 660
agtactgctt ttccaagaac antatgccc tagcgta 697

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<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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ggaggtggtt ccacacacctt g

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21

```

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
caaccagatc gagattcacc

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20

```

<210> 18
<211> 331
<212> DNA
<213> Escherichia coli

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cccatcatgt ctaacggaaa gactttcaca ttgagcaacg gcgtaagat tcctggcgtc 120
ggctttggta cttcgctag tgaaggttcc aaggggcgaga cctatactgc tgtcaccact 180
gccctgaaga ccgggttaccg tcacttggac tttgcctggt actacctgaa cgagggtgag 240
gttgggtgagg gtatccgtga cttcctgaag gagaacccct cggtaagcg tgaggacatc 300
ttcgtctgca ccaagggtgtg gaaccacctc c

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331

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<210> 19
<211> 743
<212> DNA
<213> Escherichia coli

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<222> (728)
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<222> (734)
<223> a, c, t, g, other or unknown

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caagaacatt atgcccgtgg cctactctcc tctgggctcg cagaaccagg ttcccaccac 120
cggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gccggcaacac 180
ccttgctcag gtttttattt cctgggtct ggcggcgtggc tacgtcggtc tcccccaagag 240
ctccaaacccc aagcgcatgt agtccaactt caagagcatt gagctctccg atgcccactt 300
tgaaggccatc aatggccgttg ccaagggtcg tcacttccgt ttcgtcaaca tgaaggatac 360
tttcggatat gatgtctggc ccgaggagac cgccaaagaac ctgtctgcgt gaatctctac 420
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gaaattataa aatnacaccn acnaaaaancc aaagcganag gatgatnccc aaaantttg 480  
 agggttctt gttgaaaac gtttgcantgan cccgaantga angaatacgat gancntgatt 540  
 tctccaaaaaa aaaaaaaaaaa aaaaacggtc cgccggccgct ccnnnggggg gcccgggttcc 600  
 caattcnccc cttatnattt aattttttt taanggggnc aaattccncc nnatttcnt 660  
 cnanattggc nggccgcctc caaacttctn tcntnaaagg gncccaattc ccccccattt 720  
 aantggattt cctntttacc ttt 743

<210> 20  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 20  
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21

<210> 21  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 21  
 ccagagggaga gtaggccacg g

21

<210> 22  
 <211> 417  
 <212> DNA  
 <213> Escherichia coli  
  
 <400> 22  
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 agaagaatgg ccagggttag cccaaatgg gcctgacgg caataacgtc attctcaagg 180  
 acctgaccga gaaccccgag cccacatggc gcgttatggaa gaagatttat gaggatcgca 240  
 agggccaggc cattgggtgc tccaaatggc ccattgcccga ccttgagaag atgtccaagt 300  
 tcgccaaggat catgcctcac gccaaccaga tcgagattca ccccttcctg cccaaacgagg 360  
 agctggtgca gtactgcttc tccaaagaaca ttatggccgt ggcctactct cctctgg 417

<210> 23  
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 <223> Description of Artificial Sequence: Primer  
  
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27

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<210> 24
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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29

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<210> 25
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
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21

```

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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gaattcaaca ccagtcagct c

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21

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<210> 27
<211> 786
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(783)

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1 5 10 15

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acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct 96
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
20 25 30

```

```

aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gaa gct aac agc gtt 144
Lys Val Val Asn Tyr Arg Ser Lys Glu Glu Ala Asn Ser Val
35 40 45

```

tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt	192
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly	
50 55 60	
gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att	240
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile	
65 70 75 80	
aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa	288
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu	
85 90 95	
aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc	336
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val	
100 105 110	
att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att	384
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	
115 120 125	
aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg	432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser	
130 135 140	
agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca	480
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac	528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	
aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat	624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	
195 200 205	
gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att	672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr	
225 230 235 240	
ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc	768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	
245 250 255	
caa gca gga cgc gga taa	786
Gln Ala Gly Arg Gly	
260	

<210> 28  
 <211> 996  
 <212> DNA  
 <213> Penicillium citrinum

<220>  
 <221> CDS  
 <222> (1)...(975)

<400> 28

atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct	48
Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro	
1 5 10 15	
ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc	96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	
20 25 30	
tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac	144
Tyr Thr Ala Val Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	
35 40 45	
tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	
gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	
tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	
tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
100 105 110	
ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	
ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
130 135 140	
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
145 150 155 160	
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
165 170 175	
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
180 185 190	

gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
195 200 205	
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
210 215 220	
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
225 230 235 240	
gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala	
245 250 255	
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	
260 265 270	
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac	864
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp	
275 280 285	
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc	912
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val	
290 295 300	
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc	960
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala	
305 310 315 320	
aag aac ctg tct gcg tgaatctcta cgaaattata a	996
Lys Asn Leu Ser Ala	
325	

<210> 29  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer  
 <400> 29  
 cggatccgtt cacgcagaca ggttcttgg

29

<210> 30  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 30  
gccatggcta tgtataaaga tttagaa

27

<210> 31

<400> 31  
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<210> 32  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 32  
cggatccgtt atccgcgtcc tgc

23

<210> 33  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 33  
cggatccgag cgcccaatac gcaaaccg

28

<210> 34  
<211> 348  
<212> PRT  
<213> Corynebacterium sp.

<400> 34  
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr  
1 5 10 15

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val  
20 25 30

Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro  
35 40 45

Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly  
50 55 60

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile  
65 70 75 80

Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp  
85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu  
 100 105 110

Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe  
 115 120 125

Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp  
 130 135 140

Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His  
 145 150 155 160

Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val  
 165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg  
 180 185 190

His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys  
 195 200 205

Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp  
 210 215 220

Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala  
 225 230 235 240

Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala  
 245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly  
 260 265 270

Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu  
 275 280 285

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu  
 290 295 300

Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr  
 305 310 315 320

Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly  
 325 330 335

Thr Leu Ser Gly Arg Ala Val Val Pro Gly Leu  
 340 345

<210> 35  
 <211> 1047  
 <212> DNA  
 <213> *Corynebacterium* sp.

<220>  
 <221> CDS  
 <222> (1)...(1044)

<400> 35

atg aag gcg atc cag tac acg aga atc ggc gcg gaa ccc gaa ctc acg	48
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr	
1 5 10 15	
gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc	96
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val	
20 25 30	
acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc	144
Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro	
35 40 45	
gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc	192
Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly	
50 55 60	
gca ggc aag gtc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc	240
Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile	
65 70 75 80	
gga acc aat gtc gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg	288
Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp	
85 90 95	
cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc	336
His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu	
100 105 110	
gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc	384
Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe	
115 120 125	
atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac	432
Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp	
130 135 140	
ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac	480
Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His	
145 150 155 160	
gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt	528
Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val	
165 170 175	
gtc att ggt acc ggc ggt ctc ggc cac gtc gct att cag ctc ctc cgc	576
Val Ile Gly Thr Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg	
180 185 190	
cac ctc tcg gcg gca acg gtc atc gct ttg gac gtg agc gcg gac aag	624
His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys	
195 200 205	
ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac	672
Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp	
210 215 220	

aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc	720
Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala	
225 230 235 240	
gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg	768
Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala	
245 250 255	
atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg	816
Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly	
260 265 270	
gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag	864
Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu	
275 280 285	
gct tcg gtg aca gtc ccg tat tgg ggt gcc cgc aac gag ttg atc gaa	912
Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu	
290 295 300	
ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc tcg gtg gag acc	960
Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr	
305 310 315 320	
ttc agt ctc gac aac ggt gcc gaa gcg tat cga cga ctg gct gcc gga	1008
Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly	
325 330 335	
acg ctc agc ggc cgt gcg gtt gtg gtc cct ggt ctg tag	1047
Thr Leu Ser Gly Arg Ala Val Val Val Pro Gly Leu	
340 345	

<210> 36  
 <211> 261  
 <212> PRT  
 <213> Escherichia coli

<400> 36	
Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser	
1 5 10 15	
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala	
20 25 30	
Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val	
35 40 45	
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly	
50 55 60	
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile	
65 70 75 80	
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu	
85 90 95	

Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val  
100 105 110

Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile  
115 120 125

Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser  
130 135 140

Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala  
145 150 155 160

Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr  
165 170 175

Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn  
180 185 190

Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp  
195 200 205

Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile  
210 215 220

Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr  
225 230 235 240

Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe  
245 250 255

Gln Ala Gly Arg Gly  
260

<210> 37

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
peptide

<400> 37

Trp Ile Ser Thr Lys Leu

1 5